

SEQUENCE LISTING

<110> Jin-Town Wang

Tzu-Lung Lin

<120> A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF

<160>5

<170>MICROSOFT WORD 2000

<210>SEQ ID NO:1

<211>LENGTH:5

<212>DNA

<213>ORGANISM: *Helicobacter pylori*

<400>SEQUENCE:1

ccatc 5

<210>SEQ ID NO:2

<211>LENGTH:1617

<212> DNA

<213> ORGANISM: *Helicobacter pylori*

<300>

<308>DDBJ/EMBL/Genbank : Accession No. : AB118944

<400> SEQUENCE:2

atg	act	aaa	aaa	ccg	gca	cga	aaa	att	tta	agc	ttt	tca	acc	acc	atg	cga	aac	cct	aaa	60
aga	ata	gga	caa	ttt	tta	gct	gtt	tta	gga	aag	ttt	gaa	aat	caa	atc	ctt	aaa	tct	tca	120
ata	atc	atg	caa	att	atc	aaa	tcc	gtt	ttg	gct	cat	agg	ctt	tat	aga	cct	act	tct	ctc	180
aat	caa	aat	aaa	gaa	ttg	aaa	gaa	aaa	ttt	gac	tcc	aat	gaa	tat	gtc	ttt	agc	gat	gaa	240
gag	tta	gaa	cgc	att	ata	gaa	ata	tcc	cca	caa	aat	cat	aaa	gaa	atg	ggc	ttt	gag	cat	300

```

gga tgg gaa agc cgg ttt gac act tgg tat aag ctt atg tgt gag ttt ggt ttt tgc tac 360
tat gca aaa tat gag aaa ata ctc atc agc gat agc gct aag atg ctt att ctt gct tat 420
tac aat aaa gaa aac gat gct ttt aaa gaa agc gtt gat gaa agc gta gtt ggg gct ata 480
ttt tta aac gct ctg tct aaa tat gaa gta gga aac cct tac aaa aag aat tta aac cat 540
aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa cga ctc aaa aat gcc cat cta acc 600
ccc cta tct gtc aaa gaa atc cct att tta ctt tgt tgg aaa gac gat aac gct aat ggg 660
ctt tat gac tac att att cgt tta aga caa gaa atc gtt act atc aat aaa aca gaa ttc 720
agc tac tca gat gaa ttt atc tat gaa aaa tgc cta aaa ctt tta gaa agt gtt aat aaa 780
aca cga ttt aaa atg agc caa atc act aac gaa gcc gtt gat gaa tac att aga aaa atg 840
cgt att aca gga ctt att tca ttg cgt ggt aat ggt agg ttt att gat att aat act aat 900
gaa aat aat aaa ata gat tac att tta caa acc cat aag gct ttt aaa ggg gat tat tta 960
aac gac act caa gct aac aaa ctc gcc ttt ttt aac tac atg gcg atc gtg gat agc ttt 1020
ctt gtt agt gtt act cca atc agc gct aat gag agc gtt aaa tca agc aaa ttg aat gaa 1080
cta gca aac act tat act aaa gat ttt atc aag caa gaa tta ctc att act tgt aac aag 1140
caa gaa tca aaa gat agt ttt tta aga ctc att gat aaa cct tta cgc tta gaa ttt tta 1200
agc gct att ttc ttg aaa caa cat ttt gaa aat tta agc gtg ata ccc aat tat aaa agc 1260
gat gat gaa ggc ttg ccc gta tac aca gca agc ggt aat aaa cct gat att gta gct atg 1320
gac aca aaa gcc caa agt tat ata gaa gtg agc ttg att aga gac aga agt caa agt acc 1380
ttg gaa atg ata cct att gcc aga cat tta aaa gaa ttg att aaa aat agc acc gat att 1440
aga gaa aaa ttt agt gtt ttt gta gct cca aat atc cat gat gat gcc aaa gaa tat gcg 1500
gaa ttt gcc caa ttc aaa gac aat att aat ata tgt tgt tat gct att aat gat ttt atc 1560
aaa aaa gta gaa aac agc ata gaa tgg tta cag atc aat gac cat ttg aaa gct taa 1617

```

<210> SEQ ID NO:3

<211>LENGTH:538

<212>PRT

<213> ORGANISM: *Helicobacter pylori*

<400>SEQUENCE:3

```

Met Thr Lys Lys Pro Ala Arg Lys Ile Leu Ser Phe Ser Thr Thr Met
1          5          10          15

```

Arg	Asn	Pro	Lys	Arg	Ile	Gly	Gln	Phe	Leu	Ala	Val	Leu	Gly	Lys	Phe	
			20					25					30			
Glu	Asn	Gln	Ile	Leu	Lys	Ser	Ser	Ile	Ile	Met	Gln	Ile	Ile	Lys	Ser	
		35					40					45				
Val	Leu	Ala	His	Arg	Leu	Tyr	Arg	Pro	Thr	Ser	Leu	Asn	Gln	Asn	Lys	
	50					55					60					
Glu	Leu	Lys	Glu	Lys	Phe	Asp	Ser	Asn	Glu	Tyr	Val	Phe	Ser	Asp	Glu	
65					70					75					80	
Glu	Leu	Glu	Arg	Ile	Ile	Glu	Ile	Ser	Pro	Gln	Asn	His	Lys	Glu	Met	
			85						90					95		
Gly	Phe	Glu	His	Gly	Trp	Glu	Ser	Arg	Phe	Asp	Thr	Trp	Tyr	Lys	Leu	
			100					105					110			
Met	Cys	Glu	Phe	Gly	Phe	Cys	Tyr	Tyr	Ala	Lys	Tyr	Glu	Lys	Ile	Leu	
		115					120					125				
Ile	Ser	Asp	Ser	Ala	Lys	Met	Leu	Ile	Leu	Ala	Tyr	Tyr	Asn	Lys	Glu	
	130					135					140					
Asn	Asp	Ala	Phe	Lys	Glu	Ser	Val	Asp	Glu	Ser	Val	Val	Gly	Ala	Ile	
145					150					155					160	
Phe	Leu	Asn	Ala	Leu	Ser	Lys	Tyr	Glu	Val	Gly	Asn	Pro	Tyr	Lys	Lys	
			165						170					175		
Asn	Leu	Asn	His	Asn	Asn	Pro	Phe	Lys	Leu	Leu	Leu	Ser	Leu	Leu	Lys	
			180					185					190			
Arg	Leu	Lys	Asn	Ala	His	Leu	Thr	Pro	Leu	Ser	Val	Lys	Glu	Ile	Pro	
		195					200					205				
Ile	Leu	Leu	Cys	Trp	Lys	Asp	Asp	Asn	Ala	Asn	Gly	Leu	Tyr	Asp	Tyr	
	210					215					220					
Ile	Ile	Arg	Leu	Arg	Gln	Glu	Ile	Val	Thr	Ile	Asn	Lys	Thr	Glu	Phe	
225					230					235					240	
Ser	Tyr	Ser	Asp	Glu	Phe	Ile	Tyr	Glu	Lys	Cys	Leu	Lys	Leu	Leu	Glu	
			245						250					255		
Ser	Val	Asn	Lys	Thr	Arg	Phe	Lys	Met	Ser	Gln	Ile	Thr	Asn	Glu	Ala	
			260					265					270			
Val	Asp	Glu	Tyr	Ile	Arg	Lys	Met	Arg	Ile	Thr	Gly	Leu	Ile	Ser	Leu	
		275					280					285				
Arg	Gly	Asn	Gly	Arg	Phe	Ile	Asp	Ile	Asn	Thr	Asn	Glu	Asn	Asn	Lys	
	290					295					300					
Ile	Asp	Tyr	Ile	Leu	Gln	Thr	His	Lys	Ala	Phe	Lys	Gly	Asp	Tyr	Leu	
305					310					315					320	

Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile
 325 330 335
 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser
 340 345 350
 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp
 355 360 365
 Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys
 370 375 380
 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu
 385 390 395 400
 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro
 405 410 415
 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly
 420 425 430
 Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile
 435 440 445
 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile
 450 455 460
 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile
 465 470 475 480
 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala
 485 490 495
 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys
 500 505 510
 Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu
 515 520 525
 Trp Leu Gln Ile Asn Asp His Leu Lys Ala
 530 535

<210>4

<211>780

<212> DNA

<213> ORGANISM: *Helicobacter pylori*

<300>

<308>DDBJ/EMBL/Genbank : Accession No. : AB118944

<400>4

atg	ggg	caa	gac	gct	gat	ttt	aaa	gcg	ctt	gaa	gaa	ctg	aaa	gaa	tac	ttt	aat	caa	gct	60
tta	aag	cta	gaa	gaa	aat	tat	ttt	agc	caa	cat	ttt	agc	aac	aag	ttt	ttc	agc	tat	aaa	120
gat	tgt	gtc	aaa	atc	ggg	agc	att	aga	gag	cat	ata	gaa	agc	tta	aac	tta	gat	aaa	tta	180
aat	aaa	gat	att	tta	tta	aca	agc	ctg	att	tat	tca	atg	gat	aag	ata	gct	aac	acg	gta	240
ggg	cat	tat	gaa	gct	tat	agg	aaa	aaa	gag	att	ttg	caa	gat	aga	ttt	att	ttt	gag	ctt	300
att	agc	cct	ata	aaa	cat	gat	aaa	aat	atc	atg	ata	gag	aga	aaa	aac	gct	aac	gaa	ttg	360
gct	aaa	acc	tta	aaa	ata	gac	tta	gtc	ttt	att	gat	cct	cca	tac	aat	tca	agg	caa	tac	420
agc	cgg	ttt	tat	cat	ctc	tat	gaa	aac	cta	gtg	cag	tgg	aaa	aaa	ccc	aaa	ctc	tat	gga	480
aca	gct	tta	aag	cca	tca	tgc	gag	aac	atg	agc	gaa	tat	tgc	cgc	tct	aat	gcc	aag	aaa	540
gaa	ttg	agc	gat	tta	att	gaa	aaa	cta	gat	tgt	aaa	agg	att	gct	tta	act	tat	aat	aat	600
acc	tat	aac	tct	aag	tct	agc	tct	tcg	caa	aat	aaa	ata	ggc	ttt	aaa	gat	tta	gtg	gaa	660
att	ttg	agt	caa	aaa	gga	aaa	tta	agc	gtt	aaa	gaa	aag	gct	cat	agt	ttt	ttt	aat	tca	720
gga	aaa	act	gat	ttt	aaa	gag	cat	aaa	gaa	ttt	tta	ttt	ata	gtg	gaa	gtg	aaa	cct	tga	780

<210>SEQ ID NO:5

<211>LENGTH:846

<212>DNA

<213> ORGANISM: *Helicobacter pylori*

<300>

<308>DDBJ/EMBL/Genbank : Accession No. : AB118944

<400>SEQUENCE:5

atg	cca	caa	ctc	aat	aag	cta	ttc	cca	aat	aac	att	aat	caa	ttt	att	gag	cct	ttt	gtg	60
ggg	ggg	ggg	agc	gtg	ttt	tta	aac	act	aag	gct	aag	aga	tac	tta	gct	aat	gac	ata	gat	120
act	aat	att	atc	aat	tta	cat	aaa	act	tta	agc	aag	ttc	aat	gtt	tgt	gag	ctt	ttt	gat	180
gaa	ttg	tct	aaa	att	atc	att	cat	tat	ggc	ttg	tct	ttc	tct	ttt	aag	ggg	att	atg	gcc	240
cct	gat	gaa	tta	aaa	aaa	caa	tat	ata	aaa	act	tac	tac	gcc	aaa	tac	aat	aaa	ata	gct	300
tat	gaa	aaa	cta	agg	gct	gat	ttt	aac	tcc	aat	caa	aac	aac	atg	ctt	tat	ttg	tat	ttg	360
ctt	tta	att	tat	gga	ttt	aat	cac	atg	att	aga	ttt	aat	tct	aaa	ggg	ctt	ttt	aat	tta	420

cct	gtg	ggt	aat	gtg	gat	ttc	aat	gaa	aat	gtt	tat	aat	gcc	cta	aaa	aac	tac	ata	gat	480
ttt	ata	cag	caa	aac	acc	att	att	ttt	cac	aat	gat	gat	tat	att	gat	ttt	ctt	aac	cac	540
acc	act	tat	tta	aaa	gat	gat	tat	gtt	tat	ttt	gac	ccc	cct	tat	tta	atc	tcc	aat	agt	600
gaa	tac	aac	aag	tta	tgg	gat	agc	gat	aat	gag	ata	gcc	tta	tat	ggt	gtt	tta	gat	agc	660
cta	gat	aaa	aag	gga	gtt	tta	ttt	ggt	ata	act	aat	ctt	att	tat	cac	aag	gga	gag	act	720
aat	ttt	att	tta	aaa	gaa	tgg	gct	aaa	aaa	tat	tat	att	ttt	aat	atc	aaa	agt	aat	tat	780
atc	agt	tat	aat	gac	aat	act	att	aaa	gaa	gat	agt	caa	gaa	atc	ttt	gta	act	aat	tat	840
agg	tga																			846